OSCHELE CELES

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FIGURE 1 page 1 of 3

			50	100	150	200	250	300	350	400	450	200	550	009	650	700	750	800	850	006	950	1000	1050	1100	1150	1200
			ACCCGCGCT	ACCGGGAGGT	GGCAGGCGGC	TGCCCAATGC	ACCTTTCCTT	GTGCAGAGAC	TGAGCTGCTT	GCGTGCGTAG	GGTGCATGGA	CCTGCTGGCA	ACCAGGTGTG	TGGCCCTCTG	TTTCACTAAC	AAGCACCGAA	AGTCTCACCA	TGTCCCGAGA	CAGGCAAATC	GCAGAGAAAG	TGGGTCGGTG	CACCCGCCA	TTCCTTTACT	ACTCAGCAAC	TCATCTTTCT	CACCGTCTAT
				CGCAGCCGAT	GGGCCCGAG	GCACTTTGGT	CCACCTGCCG	GGCCAGGGTT	CTTTTGGCTT	TTCACTAGTA	GCGTGTCAGT	TGCTGGTCTA	AGCTGTGCCT	CACGGATATC	TGGGCAGGAA	AGTCGCCAGG	GAGGCATCTG	GATGCTATCC	CCAACCCCAT	GGTGCCTACT	TGAGTCTCTC	CTGCTGTCAC	GACCAGACAT	CCTCATTCCT	CTGGTGGAGA	CTGCAGGACA
			ATCCCGGCCT	CTCTCTGCTG	TGCGGCGCCT	AAGATCTACC	CTCACAGCCT	AAGAGCTGGT	AACGTGCTGG	TCCCATGGCC	TTGAGACCCT	GGCGACGACC	GGTGCCCCCC	TTTGTGCCAC	ACCCGACCCG	CAAGAGCAGT	GAGGTACAAA	AAGAAGGCCA	GCAGGTGCTA	GGTCCCCCGA	GTGTCTGACC	CTCCACATCT	CATTTATTGA	CGTCTAAACC	GGCCAGGAGA	CAGGACCACT
	to 3435	3404	TGGGAGGCCC	CCGCGGTGCG	GCAACCTTTG	CGGGGACCCG	TGCACTGGGG	TCATCCCTGA	CAACGAGAGA	GAGGCGGGCC	AACACTGTTA	GAGCCGAGTG	TTTATCTTCT	CTGTACCAAA	TTACAGGCCC	TACAACAGAT	TTGCCATCTC	GCCTTCAGCT	GACCCCACAG	AGTCCTGCTC	TAAAGGAAAG	ACAAGCCCAG	CAGCTCAGGC	TGGCCAAGAG	ACTTGACTGG	CCTAGGACAT
miki cDINA clone - 3496 base pairs	-cDNA: nucleotides 10	-ORF: nucleotides 39 to	GAATTCCGGG	CCTCGTTGCC	GTGGCCGCTG	TTGTGCAACC	CTAGTGTGCA	CCACCAGGTG	TCTGCGAGCG	AACGAGGCCA	CTACTTGCCC	TGCTACTGTT	CACTGTGCTC	TGGGTCTCCC	TGTCCGCTAG	CTTAGGTTCT	ACCCCTGGCC	GTACAAGTGT	GTGGAGGAGG	ATGGGTGCCA	ATTTGTCTTC	TGCTGTAAAC	AAATGCCTTT	CCAGGGGAGA	CTCCAGCCTA	GGGCTCAAGG
	- 3496 base pairs	- 3496 base pairs - cDNA: nucleotides 10 to 3435	- 3496 base pairs - CDNA: nucleotides 39 to 3435	10 to 3435 9 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT	10 to 3435 9 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CTCTCTGCTG CGCAGCCGAT ACCGGGAGGT	10 to 3435 9 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CTCTCTGCTG CGCAGCCGAT ACCGGGAGGT GCAACCTTTG TGCGGCGCCT GGGGCCCGAG GGCAGGCGCC	10 to 3435 9 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CTCTCTGCTG CGCAGCCGAT ACCGGGAGGT GCAACCTTTG TGCGGCGCCT GGGGCCCGAG CGGGGACCCGG AAGATCTACC GCACTTTGGT TGCCCAATGC	10 to 3435 19 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CCGCGGTGCG TGCGGCGCCT GGGGCCCGAG GCAACCTTTG TGCGGCGCCC AAGATCTACC GCACCTTTGGT TGCACTGGGG CTCACAGCCT CCGCGCCCC TGCACCTTTCC TGCACTTTCC TGCACTTCCTC TGCACTTCCT TGCACTTCCT TGCACTTCCT TGCACTTCCT TGCACTTCCT TGCACTTCCTT TGCACTTCCT TGCACTTCCTT	10 to 3435 TGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CTCTCTGCTG CGCAGCCGAT ACCGGGAGGT GCAACCTTTG TGCGGCGCCT GGGGCCCGAG CGGGGACCCG AAGATCTACC GCACTTTGGT TGCCCAATGC TGCACTGGGG TGCACTGGGG TGCACTGGGG AAGAGCTGT GGCCAGGGTT GCCACCTTTCCTT TCATCCCTGA AAGAGCTGGT GGCCAGGGTT GCCACCTGCCT GGCCACCTGCCT GCCACCTGCCT GCCACCTGCCT GCCACCTGCCT TGCACTGCGCCT TGCACTGGGGCCT TGCACTGCGCT TGCACTGCCT TGCACTGCCT TCATCCCTGA TCATCCCTGA TGCACTGCCT TCATCCCTGA TCATCCCTGA TGCACTGCCT TGCACTGCCT TGCACTTTCCTT TCATCCCTGA TGCACTGCT TGCACTGCCT TGCACTGCCT TGCACTGCCT TGCACTGCCT TGCACTGCCT TGCACTGCCT TGCACTGCCT TGCACTGCT TGCACTGCT TGCACTGCT TGCACTGCT TGCACTTTCCTT TCATCCCTGA TGCACCTGCT TGCACTTTCCTT TGCACTGCT TGCACTTTCCTT TGCACTGCT TGCACTTTCCTT TGCACTGCT TGCACTTTCCTT TGCACTGCT TGCACTTTCCTT TGCACTGCT TGCACTTTCCTT TGCACTTTCCTT TGCACTGCT TGCACTTTCCTT TGCACTTCT TGCACTTTCCTT TGCACTTTCCT TGCACTTTCCT TGCACTTTCCT TGCACTTTCCT TGCACTTTCCT TGCACTTTCCT TGCACTTTCCT TGCACTTTCCT TGCACTTT TGCACTTTCCT TGCACTTT TGCACTTT TGCACTTT TGCACTT TGCACT TGCACTT TGCACTT	10 to 3435 9 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CTCTCTGCTG CGCAGCCGAT ACCGGGAGGT GCAACCTTTG TGCGCCCT GGGGCCCGAG GGCAGCGGC TGCACCTGGG AAGATCTACC GCACTTTGGT TGCCCAATGC TGCACTGGGG CTCACAGCCT CCACCTGCCG ACCTTTCCTT TCATCCTGA AAGAGCTGGT GGCCAGGGTT TGAGCTGCTT TCATCCTGA AAGAGCTGGT GGCCAGGGTT TGAGCTGCTT	10 to 3435 19 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CTCTCTGCTG CGCAGCCGAT ACCGGGAGGT GCAACCTTTG TGCGGCGCCT GGGGCCCGAG GGCAGCGGC TGCACTGGG CTCACAGCCT CCACTTGGT TGCCCAATGC TGCACTGGGG CTCACAGCCT CCACTGCCG ACCTTTCCTT TGCACTGGGG CTCACAGCTT GGCCAGGGTT TCATCCCTGA AAGAGCTGGT GGCCAGGGTT TGAGCTGCTT TCATCCCTGA AACGTGCTGG CTTTTGGCTT TGAGCTGCTT GAGCGGGCC TCCATGGCC TTCACTAGTA GCGTGCTTAGTA	10 to 3435 10 to 3435 19 to 3404 TGGGAGGCCC CCGCGGCT CCGCGGTGCG CCGCGGCT CCGCGGCCT CCGCGGCCC GCACCTTTG GCACCTTTG TGCGCGCCC AAGATCTACC CCGCGCCCGAG GCACCTTTGCT TCCCCTGGG AAGATCTACC TCACCCTGGG AAGAGCTGGT CCACCTGCCG AAGAGCTGGT GGCCAGGGT GGCCAGGGT GCACCTTTCCTT GGGCCCGAG AACACTGTGC TCACCCTGGC TCACCTGGC TCACCTGGC TCACCTGCGC TCACCTGCGC AACACGTGCTG TTCACCTGCC TCACCTGCC TCACCTGCC AACACGTGCTG TTCACCTTGCT GGCCAGGGT AACACTGTTA TTGAGACCCT GCGCGCCT GGCCAGGCT AACACTGTTA TTGAGACCCT GCGCGCCT GCCAGCCCT GCCACCTTTC AACACTGTC TTCACTAGTA GCCCGCGCT ACCCTTTCCTT GCCACCTTCCTT GCCACCTTCCTT GCCACCTTCCTT GCCACCTTCCTT AACACTTTCCTT GCCACCTTCCTT GCCACCTTCCTT GCCACCTTCCTT GCCACCTTCCTT GCCACCTTCCTT GCCCCATGCCT AACACTTTCCTT GCCACCTTCCTT GCCCCATGCCT GCCACCTTCCTT GCCCCATGCCT GCCACCTTCCTT GCCCCATGCCT AACACTTTCCTT GCCCATGCCT GCCACCTTCCTT GCCCCATGCCT GCCACCTTCCTT GCCCCATGCCT AACACTTTCCTT GCCCCATGCCT GCCCCCCCCCC	10 to 3435 9 to 3404 TGGGAGGCCC CCGCGGCT CCGCGGCT CCGCGGCGCT CCGCGGCGCCT CCGCGGCGCC CTCTCTGCTG CGGGCGCCCT CGGGGACCCG AAGATCTACC TGCACTGGG CTCACAGCCT TCACCCGGC TCACAGCCT TCACCCTGA AAGAGCTGGT CCACCGGCGC TCACAGCCT TCACCCTGA AAGAGCTGGT GGCCAGGGT AACGTGCTG AACGTGCTG AACGTGCTG AACGTGCTG AACGTGCTG AACGTGCTG AACGTGCTG AACGTGCTG AACGTGCTG CTTTTGGCT TCACCCGCCT TCACCTGCT AACGTGCTG AACGTGCTA AAC	10 to 3435 19 to 3404 TGGGAGGCCC CCGCGGTGCG CTCTCTGCTG CGCGGCGCCT CGGGGACCCG AAGATCTACC CGGGGACCCG AAGATCTACC CGCGGCGCCT TGCACTGGG AAGATCTACC CCACCTGCCG AAGATCTACC CCACCTGCCG AAGATCTACC TCATCCCTGA AACGTGCTG GCGCCCGAG GCACTTTCTT TGAGACCCT TCATCCTGA AACGTGCTG GCGCCCGAG AACGTGCTG AACGTGCTG AACGTGCTC TCATCCTTC GCGCGCCT GCGCGCCT TGAGCCGCT TGAGCCGCC ACCTTTCTT TGAGACCT TTATCTTCT GGTGCCCCC AGCTGTCCT ACCAGGTGCC AGCTGTCCT ACCAGGTGCC AGCTGTCT ACCAGGTGCC AGCTGTCT ACCAGGTGTC ACCAGGTGCC AGCTGTCCT ACCAGGTGCC AGCTGTCCT ACCAGGTGCC AGCTGTCT ACCAGGTGTC ACCAGGTGCC AGCTGTCCT ACCAGGTGCC AGCTGTCCT ACCAGGTGCC AGCTGTCC ACCAGGTGC ACCATTCCT ACCAGGCG AACATCCT ACCAGGCG AACCATCC ACCATTCCT ACCAGGCG AACATCCT ACCAGGCG ACCATTCCT ACCAGGCG AACATCCT ACCAGGCG AACATCCT ACCAGGCG AACATCCT ACCAGGCG AACATCCT ACCAGGCG AACATCCT ACCAGGCG AACATCCT ACCACGCG AACATCCT ACCACGCG AACATCCT ACCACGCG AACATCCT ACCACT ACCACGCG AACATCCT ACCACT ACCACT	10 to 3435 9 to 3404 TGGGAGGCCC TGGCGCCT CCGCGGTGCG CTCTCTGCTG CGCACCTTTG CGGGGACCCG CGGGGACCCG CGGGGACCCG CGGGGACCCG CGGGGCCCCCGAG CCACCTTTG TGCACTGGG CTCACTGGG CTCACTGCG CGGGCGCCT TGCACTGGG CTCACCGGCGC CGGGGACCCG AAGATCTACC CCACCTTGGT TGCACTGGG AAGATCTACC CCACCTGCCG AAGATCTACC TCACCGGGAGGC TCACCGGGAGGC TCACCGGGAGGC TCACCGGGAGGC AACGTGCTG CCACCTGCC ACCTTTCCTT TGAGACCCT TCACCGGGAGGC ACCTTTCCTT CCATGGCC ACCTTTCCTT TGAGACCCT TTTATCTTCT CTCCATGCC ACCTGGGCC ACCTGCGGC TTCACTAGTA CTTTTATCTTCT TTTATCTTCT TTTTTTCT TTTTTTTCT TTTTTTTT	10 to 3435 9 to 3404 TGGGAGGCCC CCGCGGTGCG CCCCGGCCT CCGCGGCGCT CCGCGGCGCT CCGCGGCGCCT CCGCGGGAGGT GCAACCTTTG GCAACCTTTG TGCACTGGGG CTCACAGCCT TGCACTGGGG AAGATCTACC CCACCGGGCCCGAG GCCAGGCGCC TGCACTGGGG AAGATCTACC TGCACTGGGG TCCACTGGCG TCCACTGGCG TCCACTGGCC TCCCATGGCC TTCATCTTT TTATCTTCT TTATCTTCT TTATCTTCT TTATCTTCT TTATCTCTC TTATCTTCT TTATCTCTC TTATCTCTC TGCGGCAGGATAT TTATCTTCT TTATCTCTC TTATCTCTC TGCGGCAGGCT TTATCTCTC TTATCTCT TTATCTCTC TTATCTCTC TTATCTCT TTATCT T	10 to 3435 9 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CTCTCTGCTG CGCAGCCGAT ACCGGGAGGT GCAACCTTTG TGCGGCGCT GGGGCCGAG GGCAGGGGC TGCAGGGCCC AAGATCTACC GCACTTTGGT TGCCCAATGC TCATCCCTGA AAGAGCTGGT GCACTTTGGT TGCCCAATGC TCATCCCTGA AAGAGCTGGT GCCCAGGGT ACCTTTCCTT TCATCCCTGA AAGAGCTGGT GGCCAGGGT TGAGCTGCT AACGTGCTG TTCACTAGTA GTGCAGAGAC ACCTTTCCTT AACGTGCTG TTCACTAGTA GTGCAGAGAC ACCTTTCCTT AACACTGTTA TTGAGCAGGCC TTCACTAGTA GCGTGCTGTA AACACTGTTA TTGAGACCCT TTCACTAGTA ACCTGTGGA AACACTGTTA TTGAGACCCT TGCTGGTCATA ACCTGTGGA AACACTGTTA TTGAGACCCT TGGTGGTGA ACCTGTGGA AACACTGTA TTTGTGCCCCC AGCTGTGCT ACCTGTGGA TTTATCTTCT TTGAGCCCCC AGCTGTGCT TTGCCATGGA <	10 to 3435 TGGGAGGCCC TGGGACCAAT TGGGAGGCCC GCACCTTGGTG GCAACCTTTG GCAACCTTTG TGCGGCGCCT TGCGGCGCCT TGCGGCGCCT TGCGGCGCCT TGCGCGGCGC TGCACCGGGAGGT TGCACTGGGG AAGATCTACC TGCACTGGGG TCACAGGCT TCACTGGCG AAGATCTACC AAGAGCTGGT GCCAGCCGCT TCACTGCCGA AAGAGCTGGT GCCAGGCGC AACACTTGGT TCACTGGCG AACACTGTG AAGAGCTGGT TTATCTTCT TTTATCTTCT TTTCATCT TTTTCATCT TTT	10 to 3435 9 to 3404 TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCGCGGTGCG CTCTCTGCTG CGCAGCCGAT ACCGGGAGCT GCAACCTTTG TGCGGCGCCT GGCAGCCGAT ACCGGGAGGC CGGGGACCCG AAGATCTACC GCACTTTGGT TGCCCAATGC TGCACTGGGG CTCACAGCCT CCACCTGCG ACCTTTCCTT TCATCCCTGA AAGAGCTGGT GCCCAGGGCG ACCTTTCCTT TCAACGAGAG AAGAGCTGGT GCCCAGGGC ACCTTTCCTT CAACGAGAG AAGAGCTGGT GCCCAGGGCC ACCTTTCCTT CAACGAGAG AAGAGCTGGT GCCCAGGGCC ACCTTCCTT AACACTGTTA AAGAGCTGGT TTCACTAGTG GCGTGCATGGA AACACTGTTA TTGACTAGT GCGTGCTCTAGT GCGTGCTGGCA AACACTGTTA TTGACTAGTC ACCTGCTGGCA ACCTGCTGGCA TTTATCTTCT GGTGCCCCCC AGCTGCTCAT ACCTGCTGGCA TTACAACAGAT ACCTGCTGGCA ACCTGCTGGCA ACCCGACCCCC TTACAACAGGCC AGCTGGCCCCC AGCTGGCACGA AGC	10 to 3435 TGGGAGGCCC TGCCGGCCT TGAGCACAAT TGGGAGGCC TCCCCGGCCT TGGGAGCCGAT TGCGGGGGGG TGCGGGGCCC TGCGGGGGCC TGCGGGGCCC TGCGGGGCCC TGCACCTTG TGCACCTGGG TGCACCTGGG TGCACCTGGG TGCACCTGGG TGCACCTGGG TGCACCTGGG TGCACCTGGC TGCACCTGGG TGCACCTGGG TGCACCTGGC TCATCCCTG TCATCCCTG TCATCCCTG TCATCCCTG TCATCCCTG TCATCCCTG TCATCCTG TCATCCCTG TCCACGGGCC TCCACGGGC TCCACGGGC TGCCGGGC TTTTTGCTT TCATCTTC TTATCTTC TTATCTTC TTACAGGCC TGCTGCTC TTACAGGCC TGCTGCTCG TGCTGCTCAC TTTACAGGCC TGCTGCTCAC TTTACAGGCC TGCTGCTCAC TTTACAGGCC TGCTGCTCAC TTTACAGGCC TGCTGCTCAC TTTACAGGCC TGCTGCCCAC TGCTGCTCT TTACAGGCC TACACACAG TTTACAGGCC TGCTGCTCAC TGCTGCTCAC TTTACCTCCAC TTTACAGGCC TGCTGCTCAC TGCTGCTCC TGCTGCTCAC TTTACCTCCCACC TGCTGCTCAC TGCTGCTCCC TGCTGCTCAC TTTCACTCCCAC TGCTGCTCCC TGCTGCTCAC TTTCACCTCCCC TGCTGCTCCC TGCTGCTCCC TGCTGCTCCC TGCTGCTCCC TGCTGCTCCC TGCTGCTCCC TGCTGCTCC TGCCCGACCC TGCTGCTCC TGCCCGACCC TGCTGCTCC TGCCCGACCC TGCTGCTCC TGCCCGACCC TGCTGCTCC TCCCCTGCTC TTTTCCTC TCCCCAACCC TCCCCGACCC TGCTGCTCC TCCCCAACCC TCCCCGACCC TCCCCGCCC TCCCCCGCCC TCCCCCCCC TCCCCCCCC	10 to 3435	10 to 3435	10 to 3435	10 to 3 435	1010 3435 105 3404	10 to 3435

FIGURE 1

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mTRT cDNA clone
- 3496 base pairs
-cDNA: nucleotides 10 to 3435
-ORF: nucleotides 39 to 3404

			7	7	, ,	, 00
CGCGTCGATA CATGCAGAGT AACAGCAAAC TCATGGATTT	CA GA GCA	BAG AGA	CCC GCC GA/	1.C.A.	3GC	CA

CTGGCAGATG GCCAATATGT CAACAGGTGA CGTCTGAGGG TCCAGAAGAA CGCCGCTTCT CAAGCTATCA ACTGGCTCCG ATACGTGGTA CAGAGCATTG GTCACAAGAG CCAGCATTTC TAGCCAAGGC GCTCCGCCTG AGCGGACAAA GACATCTACA CCAGACACCC TCTGCAGACT GTCTCTGCAA ATGCCATCCC CACTCGGAGA AACATGAGTT GATGCCAGTG TGACCTCCA

GAACACCAGC GGGAAGGACC CCTGGCAGGT AAAGAAGTTC GGCTACGTTC ATCACCAGGA AGGTCACATT TGATGTGGAA TCCAACAGCT ACACCTTGAG CTTATGGGGT GGCCTTTGTG CTGGTGGAGG GCTAGTCTCT GGTCATTCTT TTCTACCGTA CCCAAGCCCA TACCAGAGCT TCAAGACTCT TTGTTAAGGC TATCCGCCAG AGTCCTTTAG GGCCAGTTCC CTCCGTTGTC AGAGGATCCT CGGCCCCTGT CAGACTCCTC CAGATGCCTT CACAGCAGTC CTGCAGGAAC CAGCAGCCCG CAGCTGCTTA CAGGCTCTTC GAGTCAGGCA GAGGTCAGGC ACCCAGCGTC ACATCCTCAC GGACCTGGCG TTAAGAACTT CAAGTCCACA ATAGCATGGG GCACGTACTG GGTGGTGTCT GCGCTTCATC AGGATGTACT CCAGGGTAAG GCCATACATG CACTGAGGAA

GCTGGTGAAC GCAGGTTTCG	1250
CCACCGCACC	
ATATGGTTTT	4
GGGGTACCAG	₹
ATCTCGTTGG	\sim
GATGAAAGTA	Š
GTGTCCCCGC	2
CTGTTCTGGC	3
TTACATCACA	\sim
AGAGTGTGTG	2.
AGAGTGCGGC	\approx
CACCTGGCTA	~
ACGGCCTGCG	\sim
TTGGGCAGAA	5
CTTCAGCATG	$\stackrel{\sim}{\sim}$
CTTCTGTACT	5
CTGCGTGTGC	0
AGATGTGACC	S
TTGTTGCCAA	0
TATGCAGTGG	5
GAGACAGGTC	0
TTAAGCATCT	2
ATCGAGCAGA	2400

FIGURE 1

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-ORF: micleotides 39 to 3404

AAAGATTGGT GACAGGTGCT	- (GCACCCTGGT TGGTGACGC GCACCCTGGTT	AAGACAGTGG TGAACTTCCC TCCATACCAG CTGCCTGCTC		ACCTCAATTA AGACGAGCCT GACCATGCGG AACAAGCTCC	Ū	TACAAGATCT TCCTGCTTCA	GCTTCCCTTT GACCAGCGTG	TCATCTCCAG CCAAGCATCC	CCAGGAATGA CACTAAAGGC	TTGGCTCTGC TACCAGGCCT	TCTACAAATG TCTCCTGGGA	CGGAAGCTCC CAGAGGCGAC	AGCCCTAAGC ACAGACTTTC	CGCTAGATGA ACATGAAGGG	GTGGATCCGA GCTCGGTACC AAGCTT
GAATGAGAGC ACAGTGTCGT CCCCAGGGCT			AAACTTGCAG GTGGTGCAGC		TTATGCCCAG AAGCTGGGAA	TGTCACGGTC		•			•	_		CAGCTGACCC	TGTCTCCTTC	GCCGTTACTA G
GCATCTCTAT TTCCTGCGTC CCAGGGCATC	GTTTCGGAGA	CCAAGCAAAA	GGTGCATGAT GGTACCCTGG	TCCCTGGTGT	ACIACICAGG AGTGTCTTCA	GCGGTTGAAG	AGACAGTCTG	TTCCATGCAT	CCTCACATTC	CTATCCTGAA	TTTCCTCTG	GCTGGCTGCT	CAGCCCAAAA	CTTAAAGCTG	CT	

TGAGAGC	AGCAGCAGCC	TGTTTGACTT	CTTCCTGCAC	2450
GTGTCGT	AAAGATTGGT	GACAGGTGCT	ATACGCAGTG	2500
CAGGGCT	CCAGCCTATC	CACCTGCTC	TGCAGTCTGT	2550
GGAGAAC	AAGCTGTTTG	CTGAGGTGCA	GCGGGATGGG	2600
TTGTTGA	TGACTTTCTG	TTGGTGACGC	CTCACTTGGA	2650
CTTCCTCA	GCACCCTGGT	CCATGGCGTT	CCTGAGTATG	2700
CTTGCAG	AAGACAGTGG	TGAACTTCCC	TGTGGAGCCT	2750
GTGCAGC	TCCATACCAG	CIGCCIGCIC	ACTGCCTGTT	2800
TTGCTGC	TGGACACTCA	GACTTTGGAG	GTGTTCTGTG	2850
TGCCCAG	ACCTCAATTA	AGACGAGCCT	CACCTTCCAG	2900
CTGGGAA	GACCATGCGG	AACAAGCTCC	TGTCGGTCTT	2950
CACGGTC	TATTTCTAGA	CTTGCAGGTG	AACAGCCTCC	3000
CAATATA	TACAAGATCT	TCCTGCTTCA	GGCCTACAGG	3050
TGATTCA	GCTTCCCTTT	GACCAGCGTG	TTAGGAAGAA	3100
CTGGGCA	TCATCTCCAG	CCAAGCATCC	TGCTGCTATG	3150
CAAGAAT		CACTAAAGGC	CTCTGGCTCC	3200
CCGCACA	TTGGCTCTGC	TACCAGGCCT	TCCTGCTCAA	3250
TCTGTCA	TCTACAAATG	TCTCCTGGGA	CCTCTGAGGA	3300
GCTGTGC	CGGAAGCTCC	CAGAGGCGAC	AATGACCATC	3350
CTGACCC	AGCCCTAAGC	ACAGACTTTC	AGACCATTTT	3400
CTCCTTC	CGCTAGATGA	ACATGAAGGG	CGAATTCCAG	3450
TACTA	GTGGATCCGA GCT	GCTCGGTACC AAGCT		3496

FIGURE 2

1122 Amino Acids 127,979 kD pI ~ 10.4

240 160 320 LCRTHRLSRR YWQMRPLFQQ 400 560 640 800 1040 1122 VARVVQRLCE RNERNVLAFG FELLNEARGG PPMAFTSSVR SYLPNTVIET LRVSGAWMLL LSRVGDDLLV YLLAHCALYL KVVSASLWGT RHNERRFFKN NRLFFYRKSV WSKLQSIGVR QHLERVRLRE LSQEEVRHHQ DTWLAMPICR LRFIPKPNGL RPIVNMSYSM GTRALGRRKQ AQHFTQRLKT LFSMLNYERT KHPHLMGSSV LGMNDIYRTW RAFVLRVRAL DQTPRMYFVK ADVTGAYDAI PQGKLVEVVA MTRAPRCPAV RSLLRSRYRE VWPLATFVRR LGPEGRRLVQ PGDPKIYRTL VAQCLVCMHW GSQPPPADLS FHQVSSLKEL KPLALPSRGT KRHLSLTSTS SGSVCCKHKP SSTSLLSPPR NMIRHSESTY CIRQYAVVRR DSQGQVHKSF RRQVTTLSDL QPYMGQFLKH LQDSDASALR NSVVIEQSIS MNESSSSLFD LKKFISLGKY GKLSLQELMW KMKVEDCHWL RSSPGKDRVP AAEHRLRERI LATFLFWLMD TYVVQLLRSF FYITESTFQK FFLHFLRHSV VKIGDRCYTQ CQGIPQGSSL STLLCSLCFG DMENKLFAEV QRDGLLLRFV DDFLLVTPHL DQAKTFLSTL VHGVPEYGCM INLQKTVVNF PVEPGTLGGA APYQLPAHCL FPWCGLLLDT QTLEVFCDYS GYAQTSIKTS LTFQSVFKAG KVKNPGMTLK ASGSFPPEAA HWLCYQAFLL KLAAHSVIYK CLLGPLRTAQ KLLCRKLPEA TMTILKAAAD PALSTDFQTI KTMRNKLLSV LRLKCHGLFL DLQVNSLQTV CINIYKIFLL QAYRFHACVI QLPFDQRVRK NLTFFLGIIS LLVNHAECQY VRLLRSHCRF RTANQQVTDA LNTSPPHLMD LLRLHSSPWQ VYGFLRACLC VPSAKKARCY PVPRVEEGPH RQVLPTPSGK SWVPSPARSP EVPTAEKDLS SKGKVSDLSL LGSRPRTSGP LVPPSCAYQV CGSPLYQICA TTDIWPSVSA SYRPTRPVGR NFTNLRFLQQ IKSSSRQEAP QNAFQLRPFI ETRHFLYSRG DGQERLNPSF LLSNLQPNLT GARRLVEIIF

H:\CLIENT\GERON\003110US\FIGURE_2.SEQ

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FIGURE 3

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mTRT vs. hTRT amino acid alignment

MTRT MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHWGSQPPADLSFHQVS IITRT MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVS

CLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLV SLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVRSYLPNTVIETLRVSGAWMLLL SRVGDDLLV

CERAWNHSVREAGVPLGL YLLAHCALYLLVPPSCAYQVCGSPLYQICATTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLAL HLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPHAS.GPRRRLG

PAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSG PSRGTKRHLSLTSTSVPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVP...TAEKDLSSKGKVSD

TRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD.KEQLRPSFLLSSLRPSLTGARRLVETIF LSLS.GSVCCKHKPSSTSLLSPPRQNAFQLRP.FIETRHFLYSRGDGQERLNPSFLLSNLQPN LTGARRLVEIIF

LGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEE NOOVTDA LGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRFRTA......

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FIGURE 3

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mTRT vs. hTRT amino acid alignment

LNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVE EDTDPRRL VQLLRQHSSPWQVYGFVRACLRRL VPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVR

Motif T

DCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIR DCHWLRSSPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVR

Motif 1. Motif 2

QHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNG<u>LRPIVNMSYSMGTRALGRRKQAQHFTQRL</u>KTLFSML QHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG<u>LRPIVNMDYVVGARTFRREKRAERLTSRV</u>KALFSVL

Motif A

NYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTY NYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIK.PQNTY

CVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQET..SPLRDAVVIEQSSSLNEASSGLFDVFLRF CIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHF

10tif B'

Motif C Motif D

MCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH<u>AKTFLRTL</u> LRHSVVKIGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ<u>AKTFLSTL</u>

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FIGURE 3

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mTRT vs. hTRT amino acid alignment

Motif D . Motif E .

<u>VRGVPEYGCVVNLRKTVV</u>NFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNR <u>VHGVPEYGCMINLQKTVV</u>NFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQS

GFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVIS VFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIIS

DTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTL SQASCCYAILKVKNPGMTLKASGS...FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATM

TILKAAADPALSTDFQTILD 1122 TALEAAANPALPSDFKTILD 1132

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FIGURE 4

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Motif T

TRT con WL V LL FFY TE R YY RK W L I hTRT/hEST2p WLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLK mTRT WLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLE Ea_p123 WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKK Sc EST2n WLFROLIPKIIOTFFYCTFISSTVT- IVVFRHDTWNRT ITPERVEY	WL WLMSV; WLMDTY WIFEDL;	V VVVQ VVSL	LL ZLLR ZLLR ZRCF	V LL FFY TE /VVELLRSFFYVTE] /VVQLLRSFFYITES /VSLIRCFFYVTEQQ	WL V LL FFY TE WLMSVYVVELLRSFFYVTETTFQK WLMDTYVVQLLRSFFYITESTFQKN WIFEDLVVSLIRCFFYVTEQQKSYS WIFROLIPKHOTFFYCTFISSTVT-	R CNRL NRLF SKTY	R YY RK W L RLFFYRKSVWSKL RLFFYRKSVWSKL YYYYRKNIWDVIMR IVVFPHDTWART	KSVW KSVW SVWS NIWD	SKI SKI VIM	, QSIG QSIG KMS IKMS	WL V LL FFY TE R YY RK W L I WLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLK WLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLE WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKK WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKK WIFEDLVVSLIRCFFYVTEGQKSYSKTYYYRKNIWDVIMKMSIADLKK	
	VLYNSF	IIPIL	OSFI	YITE	WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFITSMKM	TVYF	RKDI	WKLL	S	FITS	MKM	

TRT con hTRT/hEST2p mTRT Ea_p123 Sc_EST2p	Motif 1 LR IPK EVRQHREARPALLTSRLRFIPKPDG EVRHHQDTWLAMPICRLRFIPKPNG KEVEEWKKSLGFAPGKLRLIPKKTT CRNHNSYTLSNFNHSKMRIIPKKSNN	Motif 2 R I KRI LRPIVNMDYVVGARTFRREKRAERLTSRV LRPIVNMSYSMGTRALGRRKQAQHFTQRL FRPIMTFNKKIVNSDRKTTKLTTNTKLLN FRIIAIPCRGADEEEFTIYKENHKNAIOP
p_Trt1p	NNVRMDTQKTTLPPAVI R LL PK KNT	FRLITNLRKRFLIKMGSNKKMLVSTNQTL

Motif A P YF K DV

P YF K DV YD I	PPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKP	QTPRMYFVKADVTGAYDAIPQGKLVEVVANMIRH	GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL	VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN	FGRKKVFVRIDIKSCVDRIKODI MFRIVKKKI KD
TRT con	hTRT/hEST2p	mTRT	Ea_p123	Sc_EST2p	Sp Trt1p

ogoverso.czies

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	Motif B'	Motif C
TRT con	KYQ GPQGSLS L Y D	LLR DDFLL IT
htrt/hEST2p	KSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGI	LLRLVDDFLLVTPHLTF
mTRT	RCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEV	LLRFVDDFLLVTPHLD(
Ea_p123	KFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFL	LMRLTDDYLLITTQENN
Sc_EST2p	KCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFK	ILKLADDFLIISTDQQQ
Sp_Trt1p	SQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFT	LLRVVDDFLFITVNK

DDFLL IT	LLRLVDDFLLVTPHLTH	LLRFVDDFLLVTPHLDQ	LMRLTDDYLLITTQENN	ILKLADDFLIISTDQQQ	LLRVVDDFLFITVNKKD
LLR	LLRL	LLRF	LMRI	ILKL	LLR

IKI con htr/hEST2p mTRT F2 p123	A F G N K AKTFLRTLVRGVPEYGCVVNLRKTVV AKTFLSTLVHGVPEYGCMINLQKTVV AVI FIEKT INIVSPENGEVENMEKT OT	W G HGLFPWCGLLL HCLFPWCGLLL
Sc_EST2p	VINIKKLAMGGFQKYNAKANRDKILA	KELEVWKHSST
Sp_Trt1p	AKKFLNLSLRGFEKHNFSTSLEKTVI	KKRMPFFGFSV

FIGURE 5 General and Murine Specific TERT Amino Acid Motifs

 $r_{17} = T > S$

x_n - any aa h = A, L, I, V, P, F, W, Mp = G, S, T, Y, C, M, Oc = D, E, H, K, R. r_1 , = I, L $r_5 = F > L$ $r_2 = R, Q$ $r_3 = Y > F$

 $r_0 = R > K$ $r_{13} = G > H$ $r_6 = P > F$ $r_{10} = G > V$ $r_{14} = C > A$ $r_7 = S > L$ $r_{11} = N > S$ $r_{15} = I > V$ $r_8 = L > M$ $r_{12} = W > F$ $r_{16} = L > V$

">" = 1st aa preferred over the 2nd

gen = general TERT motif hum = human specific motif mus = mouse specific motif

bold residues are species specific changes

Motif T

 $r_4 = K > H$

 $W - r_1 - x_4 - h - h - x - h - h - r_2 - p - F - F - Y - x - T - E - x - p - x_3 - p - x_{2 - 3} - r_3 - R - r_4 - x_2 - W$ gen $W-r_1-x_4-h-h-x-h-h-r_2-p-F-F-Y-V-T-E-x-p-x_3-p-x_{2\cdot3}-r_3-r_3-R-r_4-x_2-W$ hum $W-r_{1}-x_{4}-h-h-x-h-h-r_{2}-p-F-F-Y-I-T-E-x-p-x_{3}-p-x_{2\cdot3}-r_{3}-r_{3}-R-r_{4}-x_{2}-W$ mus

Motif 1

Motif 2 gen $h-R-h-r_1-P-K-x_2-p$ gen r_5 -R-h-I- x_2 -h hum $h-R-h-r_1-P-K-x-D-p$ hum mus $h-R-h-r_1-P-K-x-N-p$ mus

Motif A

gen $P-c-x-r_3-F-h-x-h-D-h-x_2-r_{14}-Y-D-x-r_{15}$ $P\text{-}E\text{-}x\text{-}r_{3}\text{-}F\text{-}h\text{-}x\text{-}V\text{-}D\text{-}h\text{-}x_{2}\text{-}r_{14}\text{-}Y\text{-}D\text{-}x\text{-}r_{15}$ hum mus $P-R-x-r_3-F-h-x-D-D-h-x_2-r_{14}-Y-D-x-r_{15}$

Motif B'

gen $Y-x-r_2-x_2-G-r_1-r_6-Q-G-r_7-x-r_{16}-S-x-h-r_1$ hum $Y-x-r_2-x_2-G-r_1-r_6-Q-G-r_7-I-r_{16}-S-x-h-r_1$ $Y-x-r_2-x_2-G-r_1-r_6-Q-G-r_7-S-r_{16}-S-x-h-r_1$ mus

Motif C

 $r_1-r_8-r_9-h-x-D-D-r_3-L-h-R_{15}-R_{17}$ gen hum $r_1-r_8-r_9-L-x-D-D-r_3-L-h-R_{15}-R_{17}$ mus $r_1-r_8-r_9-F-x-D-D-r_3-L-h-R_{15}-R_{17}$

Motif D

gen $r_{10}-x_2-c-x-p-x_3-r_{11}-x_2-K-x_3$ hum r_{10} - x_2 -c-x-p- x_3 - r_{11} -R-K- x_3 mus r_{10} - x_2 -c-x-p- x_3 - r_{11} - \mathbf{Q} -K- x_3

Motif E

gen r_{12} -x- r_{13} -x- r_{7} -x hum hum

FIGURE 6

page 1 of 2

100 150 200 350 400 450 500 550 600 650 700 750 800 850 900 950 1100 11100

250 300

mTRT Promoter Region -cDNA start at 1680 -ORF start at 1709

GGCAAGCGCC GCTAACGCAG TAGACAATTT CCTAAATTTC AGGTCGGTGG AGCAGAGCTG GAGATGATGC ACGGAACATA AAAGCAGGCC AACTAAGCCA TATGGCTCAG AAGGTAGCTT AAACGGACTT NTACTTCCCA GAGACTGTTT CATTGTTGGC GCAGACTTCC ACAGATTCCC **LTGGATTCTG TATATTTGTT** CTATCCTACC CCTTCTTTT TTTTATTTT

CTCACCCAAT GGCTTTTACC ACAAGTGTGC CTAAAATAGC ATAGAAGCAA TCTGGACTCT **LTTGGGATCT** AGCATGTAGT CCATCCTAAG TATAAGGGAG AGTCGTGTCA CCACTTGTTI AGAGTAGCTA TCTATGCTGG AATCTTCAAA TGTAACACAA ATGCTTGAAC ATAAATTTCT AGCATTTCAG TATTCCCAG GAGACTGTTT CCGCCTCAC CTTGGTTTT

CAGTTCAG TAAATATG TTTCCTCA AGGTCCTTI CCAGGTTG ACAAGTGT ACCACCAT TTTCTTTG CAAACCCC TCCCTGTA IGTTTGCC/ AGATTCAA GTCGAGGT **LTGAGGCA** GGCTGGT TCTATGCT TTACATAT ACGTGCAA GGCCCTC GAGGTGA GGAGTGT TCCACTT TAGGTC

TCGTGGCTGG TCGGTTGTTA TGCACCCCTT CCCAAGTGGA TCATCCTGCT	CCCGCGATAT GAACTACACT TCTTATTTTT AAGGTAGCTT	GATGTCCACT TACCAAGGCG TTCAAATGCT CACCAAAGGT AGTAGAGATC	CCTCTCTAAC ACCCCCACCC TTGCCAACCT TGTGTGCACA TGTGTGCACA AGTGAAAAA GTGGGTGTTT AATAAAGCCT
TCCTGGTTTA TTTTTCTAC AGTCAGCAAG TCTCATTTTG GAATGCTTTT	ACCACCATGC TTTCTTTGGG CCCGCGATAT GAACTACACT CCATATCTCT	CAAAAAGACT CCTGAGCATT AACGCGCCTG AAGCTGAAGG ACTCAGCTAC	TTCAGCAGCC CCCAACAACA ACTATCACAG CCGCTTTGGC TTGCTATGGG CCACTGGAAC TCCTTTGGTG
rt CAG GG GG	76C 66 76C 66	CTT NAT SAA GA AA	AA GC GT FCG AGG AGG

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TAACCTATAT	AGTA
CACCACCAC	CTCA(
CTCAGGAACA	GGCA
ATCAAGGATA	GGCT
CCTGGGGATT	CCCA
AGAGGGAAAT	CCTG
AGCAACCACT	GAAC
ATTGTGACCA	TCAA
CTACAACGCT	TGGT
CATCTTTTC	GTCGT
AGCACACCCT	TGCA
TGAGCACAAT	GACC
CGCAGCCGAT	ACCG(
9222999	

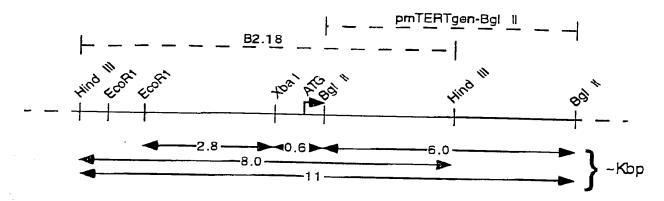
GTGT
TAG
CTTC
OGCC
$^{\mathrm{TGC}}$
GGGC
AGT
GAA
CTCA
TTCC
CCTC
GTG(

CAGCTGTAA	TCATTAAGAA	CTGAGATTGC
IGTCAACCA	CAGCAGGCTG	GAGCAGTCAG
AGGTCCTCC	GCCTACCTAA	CCTTCAATAC
TTGCCCAAA	CCTCGCCCCA	GTCTAGACCA
GCGAAAAGG	AAGCCCGAGA	AGCATTCTGT
LCCCCCT	TTCGTTACTC	CAACACATCC
GGGAACACA	CCTGGTCCTC	ATGCACCAGC
GTACTATTG	CTGCGACCCC	GCCCCTTCCG
AATCCCGCC	CCTTCCTCCG	TTCCCAGCCT
CAGTGGCC	TGGGTCCTGG	CTGTTTTCTA
TCCCGCACG	TGGGAGGCCC	ATCCGGCCT
CTCGTTGCC	CCGCGGTGCG	CTCTCTGCTG
TGGCCGCTG	GCAACCTTTG	TGCGGCGCCT

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FIGURE 7 mTERT Genomic DNA

lambda-mTERT (~23 Kbp)



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FIGURE 8 page 1 of 2

Preliminary sequence of B2.18, containing the promoter region of mTERT. CDNA starts at: 2057

ORF starts at: 2087

AAACAAAGTC	AATGAGGAAT	GGCTGTGTTC	CATCTTGACC	ACTGAGAAGT	50
AAAACCGGGT	GCAGTGATGT	CCAAAAAGGC	AAGGTGACAG	CAGAGCGGAG	100
GCCCCAATCT	AGAGCAGGGC	CTTCGGTTTG	AATGGGGGAG	ATCAAACGGG	150
AGTTGGTTTC	TGCCAGCACG	TTGGGGTAGA	AGGTGGAACA	TGAAAGGTCC	200
CCGAGGATTT	CGAGAGTCCA	TAGGGGTAGC	GACACCCGAG	GTCTTCTTT	250
TCACCTCCTT	CCCTGCAGGG	GAGATGACTT	TTACCACAGT	CGTTTATGGG	300
AAAGTTCCTA	GGGGCAGCCC	CTCCCCAAAA	AGGCTCTCCC	TGGCCTCATG	350
TTTCAAAGCA	CAGCTTTTTA	AAGCAGGCCT	GTTAAGCACA	AAGGATCCCG	400
AATCCTGGCT	TCATCGTTGG	CTGGTAGACA	ACTTCCACTC	GTTTTCCACT	450
TCAGTITCIT	CTAACTCTGT	TGTTATTTGA	TTCTGATGCT	TGAACCCAGG	500
GTTGTGTAGT	CAGCAAGTGC	TACCCCCTCC	TCCTCTTCTT	TGTTTTTTG	550
AGGCAGGGTC	TCATTTTGCC	CAAGTGGACC	TAAATTTCAG	CATGTAGCTG	009
GCCTGGTTTT	GAATGCCTTC	TCATCCTGCC	TCTACTTCCC	AAGAGTAGCT	650
TACAAGTGTG	CACCACCATG	CCCCGCGATA	TTCTTATTT	TGAGACTGTT	700
TTCTATGCTG	GTTTCTTTGG	GGAACTACAC	TAAGGTAGCT	TACAAGTGTG	750
CACCACCATG	CCCCGCGATA	TTCTTATTT	TGAGACTGTT	TTCTATGCTG	800
GTTTCTTTGG	GGAACTACAC	TAAGGTAGCT	TCATTGTTGG	CATAAATTTC	850
	CCCATATCTC	CTAAGTAGCA	GAACTAAGCA	AATCTCAAAC	900
	AAAAGACTGA	TGTCCACTAA	ACGGACTTCT	AAAATAGCTC	950
CCTGTAATCC	TGAGCATTTA	CAAGGCGGCA	GACCICCTAT	AAGGGAGTAA	1000
ATATGAAAAC	GCGCCTGTTC	AAATGCTAGG	TCGGTGGATA	GAAGCAATTT	1050
CCTCAGAAAG	CTGAAGGCAC	CAAAGGTTAT	ATTTGTTAGC	ATTTCAGTGT	1100
	CAGCTACAGT	AGAGATCACA	GATTCCCTAT	TTCCCAGAGA	1150
	AGCAGCCCCT	CTCTAACTAT	GGCTCAGAGT	CGTGTCATTA	1200
•	AACAACAACC	CCCACCCCTA	TCCTACCCC	GCCTCACACG	1250
•	ATCACAGTTG	CCAACCTAGC	AGAGCTGCCA	TCCTAAGGTC	1300
_	CTTTGGCTGT	GTGCACAGGC	AAGCGCCCTC	ACCCAATGGC	1350
CCTGGCCTTG	CTATGGGTGC	GTGAGTTGAG	ATGATGCTCT	GGACTCTGAG	1400

DSCHEHSO.CSCS

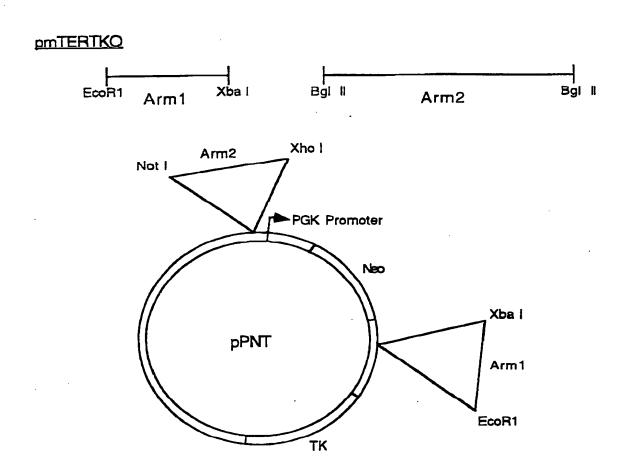
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GTGAAGGCCA	CTGGAACAGT	GAAAAAAGCT	AACGCAGGG		140
GICCCTICC	TTTGGTGGTG			SELECTION OF STREET	1 ± 00
GTGTATGGTC	GCACCACAAT	AAAGCCTTAA		AGAATTTCAG	1550
CTGTAATCAT	TAAGAACTGA	GATTGCCACC	ACCCACCTCA	CTGTCTGTGT	1600
CAACCACAGC	AGGCTGGAGC	AGTCAGCTCA	GGAACAGGCA	AAACCTTAGG	1650
TCCCTCCGCC	TACCTAACCT	TCAATACATC	AAGGATAGGC	TTCTTTGCTT	1700
GCCCAAACCT	CGCCCCAGTC	TAGACCACCT	GGGGATTCCC	AGCTCAGGGC	1750
SAAAAGGAAG	CCCGAGAAGC	ATTCTGTAGA	GGGAAATCCT	GCATGAGTGC	1800
GCCCCTTTC	GTTACTCCAA	CACATCCAGC	AACCACTGAA	CTTGGCCGGG	1850
SAACACACCT	GGTCCTCATG	CACCAGCATT	GTGACCATCA	ACGGAAAAGT	1900
ACTATTGCTG	CGACCCCGCC	CCTTCCGCTA	CAACGCTTGG	TCCGCCTGAA	1950
rcccccccT	TCCTCCGTTC	CCAGCCTCAT	CTTTTTCGTC	GTGGACTCTC	2000
AGTGGCCTGG	GICCIGGCIG	TTTTCTAAGC	ACACCCTTGC	ATCTTGGTTC	2050
CGCACGTGG	GAAGGCCCAT	CCCGGCCTTG	AGCACAATGA	CCCGCGCICC	2100
rcgrigaacc	GCGGTGCGCT	CTCTGCTGCG	CAGCCGATAC	CGGGAGGTGT	2150
BGCCGCTGGC	AACCTTTGTG	CGGCGCCIGG	GGCCCGAGGG	CAGGCGGCTT	2200
TGCAACCCG	GGGACCGAAG	ATCTACCGCA	CTTTGGGTTG	CCCAATGCCT	2250
AGTGTGCATG	CACTGGGGCT	CACAGCCTCC	ACCTGCCGAC	CTTTCCTTCC	2300
ACCAGGTGGG	CCTCCAGGCG	GGATCCCCAT	GGGTCAGGGG	CGGAAAGCCG	2350
SGAGGACGTG	GGATAGTGCG	TCTAGCTCAT	GTGTCAAGAC	CCTCTTCTCC	2400
TACCAGGTG	TCATCCCTGA	AAAGAGCTGG	TGGCCAGGGT	TGTGCAGAGA	2450
TCTGCGAGC	GCAACGAGAG	AAACGTGCTG	GCTTTTGGCT	TTGAGCTGCT	2500
AACGAAGCC	AGAAGCGGGC	CTCCCATGGC	CTTCACTAAT	TAGCGTGCGT	2550
AGCTACTTG	CCCAACACTG	TTATTGAAAA	CCTGCGTGTC	AGTGGTGCAT	2600
GATGCTACT	GTTGAGCCGA	ATGGGCGACA	CCIGCIGGIC	TACCTGCTGG	2650
					2651





FIGURE 9 mTERT Genomic DNA



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